



PCT

RAW SEQUENCE LISTING

DATE: 03/27/2003

PATENT APPLICATION: US/09/914,006D

TIME: 12:10:04

Input Set : A:\914,006s1.txt

Output Set: N:\CRF4\03272003\I914006D.raw

3 <110> APPLICANT: Eggeling, Lothar
 4 Sahm, Hermann
 6 <120> TITLE OF INVENTION: METHOD FOR MICROBIALY PRODUCING L-VALINE
 8 <130> FILE REFERENCE: 5899*13
 10 <140> CURRENT APPLICATION NUMBER: 09/914006D
 C--> 11 <141> CURRENT FILING DATE: 2003-08-21
 13 <150> PRIOR APPLICATION NUMBER: PCT/EP00/01405
 14 <151> PRIOR FILING DATE: 2000-02-21
 16 <160> NUMBER OF SEQ ID NOS: 7
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2952
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Corynebacterium glutamicum
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 30 ctgaaacctc acatcgtgat aaccctgcgt cacagcacta gagtgtata agccgtccga 180
 32 accaaaggtc cacacctctg cagcagtaga agctcaccca agttttcaaa gtgccgttga 240
 34 ttcttgacaa ccaccgcgcg ctcttttagag cagatttgaa aagcgcata tgatcccact 300
 36 tcgttcaaaa gtcaccaccg tcggtcgcaa tgcagctggc gctcgcgcc tttggcgtgc 360
 38 caccggcacc aaggaaaatg agttcggcaa gccaatgtt gccatcgtaa actcctacac 420
 40 ccagttcgtg cccggacacg ttcaccttaa gaacgtcggc gatattgtgg cagatgcagt 480
 42 gcgcaaaagcc ggtggcggtc caaaggaatt caacaccata gtcgatgacg gcacgcgat 540
 44 gggacacggc ggcagtgtgt actcctgcc atcccgtaa atcatcgccg actccgctga 600
 46 atacatggtc aacgcacaca ccgccgacgc catggtgtgt atctccaact gtgacaagat 660
 48 caccgccaggc atgctcaacg cagcaatgcg cctgaacatc ccagtgggtc tcgtttccgg 720
 50 tggcccaatg gaagctggca aggtgtcgt cgttgagcgc gttgcacacg caccaaccga 780
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 60 ccgccgctac tacggtgaag aagacgaatc cgttctgcca cgtggcattg ccaccaagaa 1080
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84 atcagggtgga ccaggcatgc aggaaatgct tcaccaacc gcattcctca agggatccgg 1800
86 cctgggcaag aagtgtgcac tgatcaccga cggccgtttc tccggagggtt cctcaggact 1860
88 gtccatcggc cacgtctccc cagaagcagc acacggcgga gtcattgggtc tgatcgaaaa 1920
90 cggcgacatc gtctccatcg acgttcacaa ccgcaagctc gaagttcagg tctccgacga 1980
92 ggaactccag cgccgcccgc acgctatgaa cgctccgag aagccatggc agccagtcaa 2040
94 ccgtaaccgc gttgtcacca aggcactgcg cgcatacgca aagatggcta cctccgctga 2100
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129 <212> TYPE: PRT
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135 1 5 10 15
138 Gly Ala Arg Ala Leu Trp Arg Ala Thr Gly Thr Lys Glu Asn Glu Phe
139 20 25 30
142 Gly Lys Pro Ile Val Ala Ile Val Asn Ser Tyr Thr Gln Phe Val Pro
143 35 40 45
146 Gly His Val His Leu Lys Asn Val Gly Asp Ile Val Ala Asp Ala Val
147 50 55 60
150 Arg Lys Ala Gly Gly Val Pro Lys Glu Phe Asn Thr Ile Val Asp Asp
151 65 70 75 80
154 Gly Ile Ala Met Gly His Gly Gly Met Leu Tyr Ser Leu Pro Ser Arg
155 85 90 95
158 Glu Ile Ile Ala Asp Ser Val Glu Tyr Met Val Asn Ala His Thr Ala
159 100 105 110
162 Asp Ala Met Val Cys Ile Ser Asn Cys Asp Lys Ile Thr Pro Gly Met
163 115 120 125
166 Leu Asn Ala Ala Met Arg Leu Asn Ile Pro Val Val Phe Val Ser Gly
167 130 135 140
170 Gly Pro Met Glu Ala Gly Lys Ala Val Val Val Glu Arg Val Ala His
171 145 150 155 160
174 Ala Pro Thr Asp Leu Ile Thr Ala Ile Ser Ala Ser Ala Ser Asp Ala
175 165 170 175

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178 Val Asp Asp Ala Gly Leu Ala Ala Val Glu Arg Ser Ala Cys Pro Thr
179      180      185      190
182 Cys Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys Leu
183      195      200      205
186 Thr Glu Ala Leu Gly Leu Ser Leu Pro Gly Asn Gly Ser Thr Leu Ala
187      210      215      220
190 Thr His Ala Ala Arg Arg Ala Leu Phe Glu Lys Ala Gly Glu Thr Val
191 225      230      235      240
194 Val Glu Leu Cys Arg Arg Tyr Tyr Gly Glu Glu Asp Glu Ser Val Leu
195      245      250      255
198 Pro Arg Gly Ile Ala Thr Lys Lys Ala Phe Glu Asn Ala Met Ala Leu
199      260      265      270
202 Asp Met Ala Met Gly Gly Ser Thr Asn Thr Ile Leu His Ile Leu Ala
203      275      280      285
206 Ala Ala Gln Glu Gly Glu Val Asp Phe Asp Leu Ala Asp Ile Asp Glu
207      290      295      300
210 Leu Ser Lys Asn Val Pro Cys Leu Ser Lys Val Ala Pro Asn Ser Asp
211 305      310      315      320
214 Tyr His Met Glu Asp Val His Arg Ala Gly Arg Ile Pro Ala Leu Leu
215      325      330      335
218 Gly Glu Leu Asn Arg Gly Gly Leu Leu Asn Lys Asp Val His Ser Val
219      340      345      350
222 His Ser Asn Asp Leu Glu Gly Trp Leu Asp Asp Trp Asp Ile Arg Ser
223      355      360      365
226 Gly Lys Thr Thr Glu Val Ala Thr Glu Leu Phe His Ala Ala Pro Gly
227      370      375      380
230 Gly Ile Arg Thr Thr Glu Ala Phe Ser Thr Glu Asn Arg Trp Asp Glu
231 385      390      395      400
234 Leu Asp Thr Asp Ala Ala Lys Gly Cys Ile Arg Asp Val Glu His Ala
235      405      410      415
238 Tyr Thr Ala Asp Gly Gly Leu Val Val Leu Arg Gly Asn Ile Ser Pro
239      420      425      430
242 Asp Gly Ala Val Ile Lys Ser Ala Gly Ile Glu Glu Glu Leu Trp Asn
243      435      440      445
246 Phe Thr Gly Pro Ala Arg Val Val Glu Ser Gln Glu Glu Ala Val Ser
247      450      455      460
250 Val Ile Leu Thr Lys Thr Ile Gln Ala Gly Glu Val Leu Val Val Arg
251 465      470      475      480
254 Tyr Glu Gly Pro Ser Gly Gly Pro Gly Met Gln Glu Met Leu His Pro
255      485      490      495
258 Thr Ala Phe Leu Lys Gly Ser Gly Leu Gly Lys Lys Cys Ala Leu Ile
259      500      505      510
262 Thr Asp Gly Arg Phe Ser Gly Gly Ser Ser Gly Leu Ser Ile Gly His
263      515      520      525
266 Val Ser Pro Glu Ala Ala His Gly Gly Val Ile Gly Leu Ile Glu Asn
267      530      535      540
270 Gly Asp Ile Val Ser Ile Asp Val His Asn Arg Lys Leu Glu Val Gln
271 545      550      555      560
274 Val Ser Asp Glu Glu Leu Gln Arg Arg Arg Asp Ala Met Asn Ala Ser

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275          565          570          575
278 Glu Lys Pro Trp Gln Pro Val Asn Arg Asn Arg Val Val Thr Lys Ala
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286 Arg Gln Val Asp
287          610
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291 <211> LENGTH: 2164
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300 agtttctaag gcaactgcaa cgaggtatct tagaactctc cgagaaatgg aattagttca      180
302 cgaggtcagc aaacgccctt tgcggtttgc gctcacggat aaaggtcgtg agatagtagg      240
304 tcttgaggta aaaatttgac tccataacga gaacttaac gagcaacacc cctgaacagt      300
306 gaatcaaata ggaattttatt tattctgagc tgggtcatcac atctatactc atgccccatgt      360
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312 gcgtcgatat gctccttggt ggtgattccg ctgccaacgt tgtgctgggt cgcgatacca      540
314 ccttgtcgat caccttggat gagatgattg tgctggccaa ggcggtgacg atcgctacga      600
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318 cgggtggagtc cgcgatccgg gtcatgcgtg aaacgggtgc ggctgcggtg aagatcgagg      720
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322 gccacatcgg gtacaccccg cagtcggagc attccttggg cggccacgtg gttcagggtc      840
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328 ccatcaccac tatcggaata ggtgccggca atggcacaga tgggcagggt ttggtgtggc      1020
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336 cgcctcctc caccacaaat ccgtcgggct cgtccccacc atgggtgcgc tacacagcgg      1260
338 acacgcctcg ttggttaaag cagcacgcgc tgaaaacgac actggtgtag ccagtatttt      1320
340 tgtcaatccc ctgcagtttg aagcactcgg tgattgcgat gattaccgca actatccccg      1380
342 ccaactcgac gccgatttag cactgcttga agaggcagg gtggatattg tgttcgcacc      1440
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352 cgttccgatt attcgtggcg ccgatggctt agccgaatcc agccgcaatc aacgtctttc      1740
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356 aaaagcagct ggtgaagcgc tagatatcca aggtgcgcgc gacaccttgg ccagcgccga      1860
358 cggcgtgcgc ttggatcacc tggaaattgt cgatccagcc accctcgaac cattagaaat      1920
360 cgacggcctg ctacccaac cagcgttggg ggtcggcgcg attttcgtgg ggccgggtcg      1980
362 gttgatcgac aatatcgagc tctagtacca accctgcgtt gcagcacgca gtttcgcata      2040
364 acgcgtgctc agctcagtgt ttttaggtgc gcggtgcgga tcggaaccgg gagttggcca      2100
366 ctgcggtggc gtggcctcac ccgacagcgc ccatgccgcc tgacgagctg cacccaacgc      2160
368 caca

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371 <210> SEQ ID NO: 4
372 <211> LENGTH: 271
373 <212> TYPE: PRT
374 <213> ORGANISM: Corynebacterium glutamicum
376 <400> SEQUENCE: 4
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382 Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr
383 20 25 30
386 Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
387 35 40 45
390 Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
391 50 55 60
394 Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
395 65 70 75 80
398 Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
399 85 90 95
402 Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
403 100 105 110
406 Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
407 115 120 125
410 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly
411 130 135 140
414 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val
415 145 150 155 160
418 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg
419 165 170 175
422 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro
423 180 185 190
426 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile
427 195 200 205
430 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln
431 210 215 220
434 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu
435 225 230 235 240
438 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile
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442 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
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447 <211> LENGTH: 279
448 <212> TYPE: PRT
449 <213> ORGANISM: Corynebacterium glutamicum
451 <400> SEQUENCE: 5
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458 20 25 30
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VERIFICATION SUMMARY

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